

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<150> US 60/092,936

<151> 1998-07-15

<150> US 09/352,168

<151> 1999-07-12

<160> 33

<170> FastSEQ for Windows Version 3.0

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<211> 372

<212> DNA

<213> *Exophiala spinifera*.

<220>

<221> misc_feature

<222> (346)...(346)

<223> n = A,T,C or G

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt	180
ggaggacgcc cgagaagcct tggtcgcgcc accacggctt gtcccatacg aagactatct	240
tgctatagta gccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc	360
ggaacacggc gc	372

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<211> 182

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<213> *Exophiala spinifera*.

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tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc	120
gacgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
ac	182

<210> 3

<211> 29

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide for 3' RACE, N21965

 <400> 3
 tggtttcggt accgacaacc ttgtatccc 29

 <210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

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 <223> Designed oligonucleotide for 5' RACE, N21968

 <400> 4
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 <210> 5
 <211> 1389
 <212> DNA
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 <222> (1)...(1386)

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 1 5 10 15

 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30

 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45

 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95

 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
210 215 220	
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala	
225 230 235 240	
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
245 250 255	
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu	
260 265 270	
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
275 280 285	
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
290 295 300	
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln	
305 310 315 320	
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	

340	345	350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac			1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp			
355	360	365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg			1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
370	375	380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga			1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
385	390	395	400
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg			1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser			
405	410	415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg			1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr			
420	425	430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa			1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln			
435	440	445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca			1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
tag			1389
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<211> 462			
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<213> Exophiala spinifera			
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35 40 45			
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
50 55 60			
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu			
65 70 75 80			
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85 90 95			
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100 105 110			
Val Ala Ser Ala Leu Ala Glu Leu Pro Val Trp Ser Gln Leu Ile			
115 120 125			
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130 135 140			
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145 150 155 160			

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 7
 <211> 1442
 <212> DNA
 <213> *Exophiala spinifera*

<220>
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 <222> (1)...(646)

<221> intron
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
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gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggg aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgctgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
210 215	
tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776

Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	
				230					235					240		
att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	824
Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	
			245					250				255				
gtg	ttc	cga	agc	aaa	aag	gtg	gtg	ggt	tcg	tta	ccg	aca	acc	ttg	tat	872
Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	
		260					265					270				
ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	920
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	
	275					280					285					
gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	968
Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	
290					295					300					305	
gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	1016
Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	
			310						315					320		
agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	1064
Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	
			325					330					335			
cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	1112
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	
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tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	1160
Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	
	355					360					365					
ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	1208
Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	
370					375					380					385	
aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	1256
Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	
				390					395					400		
ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	1304
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	
			405					410					415			
ctc	aga	acg	ccg	ttc	aag	agt	ggt	cat	ttc	ggt	gga	acg	gag	acg	tct	1352
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	
		420					425					430				
tta	ggt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	1400
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	
	435					440					445					
ggt	gct	gca	gaa	ggt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag			1442
Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala				
450					455					460						

<210> 8
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 <212> PRT
 <213> *Exophiala spinifera*

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400

Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser
				405					410					415	
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr
			420					425					430		
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln
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	450					455					460				

<210> 9
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 <212> PRT
 <213> *Exophiala spinifera*

<400> 9

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Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
			20					25					30		
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
		35				40						45			
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50				55						60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65				70					75					80	
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
			85					90					95		
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105					110		
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
		115				120					125				
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	130				135				140						
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145				150					155					160	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
			165					170					175		
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
		180					185					190			
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
		195				200						205			
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Ala	Cys	Gly	Val	Val	Ser	Gly	Gly
	210				215						220				
Gly	Leu	Val	Ser	Gln	Trp	Ser	Phe	Gln	Val	Cys	Ser	Arg	Phe	Ala	Met
225				230					235					240	
Pro	Cys	Gln	Arg	Asn	Leu	Phe	Gln	Ala	Gln	Cys	Thr	Ser	Thr	Pro	Pro
			245					250					255		
Ser	Leu	Lys	Leu	Ser	Ser	Arg	His	Pro	Ala	Val	Gln	Tyr	Asp	Arg	Pro
		260					265					270			
Arg	Ala	Pro	Cys	Ser	Glu	Ala	Lys	Arg	Trp	Trp	Phe	Arg	Tyr	Arg	Gln
		275				280						285			
Pro	Cys	Ile	Pro	Pro	His	Phe	His	His	Leu	Phe	Pro	Pro	Arg	Ser	Lys
		290			295						300				
His	Trp	Arg	Lys	Ile	Leu	Ser	Trp	Ala	Thr	Ile	Ala	Arg	Ser	Ser	Tyr
305				310					315						320
Gly	Thr	Ser	Arg	Gly	Gly	Ala	Asn	Lys	Ala	Ser	Arg	Ala	Ser	Ser	Asn
			325					330					335		
Arg	Ala	Val	Thr	Pro	Ser	His	Leu	Pro	Glu	Ile	Pro	Ala	Ser	Thr	Ser

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	

340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg			1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag			1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa			1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca			1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	
tag			1392

<210> 11
 <211> 463
 <212> PRT
 <213> *Exophiala spinifera*

<220>
 <223> Extra lysine in the polypeptide sequence of
 K:trAPAO, 463 aa.

<400> 11

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20				25						30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35				40					45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
50					55				60						
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65				70					75					80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
			85				90						95		
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
		100				105						110			
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115				120						125			

Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135				140					
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
210						215				220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
290						295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310				315						320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330						335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
370						375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405				410						415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440					445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
450						455					460				

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12

ggggaattca aagacaacgt tgcggacgtg gtag

34

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors, N23259

<400> 13
ggggcgggccg cctatgctgc tggcaccagg ctag 34

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
tggtttcggt accgacaacc ttgtatccc 29

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' race, N21968

<400> 15
gagttggtcc cagacagact tttgtcgt 28

<210> 16
<211> 1673
<212> DNA
<213> Exophiala spinifera

<220>

<221> sig_peptide
<222> (1)...(267)
<223> yeast alpha mating factor secretion signal.

<221> CDS
<222> (1)...(1662)

<400> 16
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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
-85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
-70 -65 -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
-55 -50 -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta	240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg	288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc	336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat	384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
cgt gta ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg	432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc	480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag	528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	
155 160 165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac	816
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	

ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
315 320 325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
330 335 340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
345 350 355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
360 365 370 375	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
380 385 390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
410 415 420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584

Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	
425						430					435					
aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	caa	cga	ggg	gct	gca	1632
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	
440					445					450					455	
gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	taggcggccg	c					1673
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala							
				460					465							

<210> 17
 <211> 554
 <212> PRT
 <213> *Exophiala spinifera*

 <220>
 <221> SIGNAL
 <222> (1)...(89)
 <223> yeast alpha mating factor secretion signal.

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	
			-85						-80					-75		
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
		-70					-65						-60			
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
	-55						-50				-45					
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	-40					-35				-30						
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
-25				-20				-15							-10	
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala	
			-5					1				5				
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	
	10					15					20					
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	
	25				30					35						
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	
40				45					50						55	
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	
			60					65						70		
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	
		75					80					85				
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	
	90					95					100					
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	
	105				110						115					
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	
120					125					130					135	
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	
			140					145						150		
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	
		155					160						165			
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	
	170					175					180					
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	

185						190						195			
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg
200					205					210					215
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu
				220					225					230	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln
			235					240					245		
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg
		250					255					260			
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
	265					270					275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280					285					290					295
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro
			300						305					310	
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
			315					320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
	330					335						340			
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
	345					350				355					
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360					365					370					375
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
			380						385					390	
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
		395						400					405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
	410					415						420			
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
	425					430					435				
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
440					445					450					455
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
			460					465							

<210> 18
 <211> 2079
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(2076)

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker; 688-2076,
 K:trAPAO; 2077-2079, stop codon. For bacterial
 expression.

<221> misc_feature
 <222> (1)...(687)
 <223> gst fusion + polylinker

<221> misc_feature
 <222> (688)...(2076)
 <223> K:trAPAO

<221> misc_feature
 <222> (688)...(690)
 <223> Extra lysine

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<400> 18
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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1             5             10             15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
             20             25             30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
             35             40             45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
             50             55             60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
             65             70             75             80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
             85             90             95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
             100            105            110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
             115            120            125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
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ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
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gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
             165            170            175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
             180            185            190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc      624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
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acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt      672

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Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly		
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gct	ggc	ttg	agc	ggc	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggc	768	
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly		
				245					250					255			
ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	816	
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr		
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Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly		
		275					280					285					
gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	912	
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe		
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gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	960	
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser		
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atc	cat	caa	gca	caa	gac	ggc	aca	acc	act	aca	gct	cct	tat	ggc	gac	1008	
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp		
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tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	1056	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro		
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Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala		
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agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	1152	
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Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile		
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Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe		
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ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggc	ctc	agt	aat	att	ttc	tcg	1296	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser		
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gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	ggc	atg	cag	1344	
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln		
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Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
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ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
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ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
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gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgc aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	
ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
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gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
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gtg cca gca gca tag
Val Pro Ala Ala
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2079

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230-692

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
225 230 235 240
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
245 250 255
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
260 265 270
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
275 280 285
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
290 295 300
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
305 310 315 320

Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp
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Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro
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Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala
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Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	370					375					380				
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile
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Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe
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Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser
		420						425					430		
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln
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Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr
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Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val
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Ser	Leu	Pro	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	
			500				505					510			
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Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly
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Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg
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Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met
			565					570					575		
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg
		580						585					590		
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly
		595					600					605			
Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys
	610					615					620				
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp
625					630					635					640
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His
			645					650					655		
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly
		660					665					670			
Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu
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 <222> (1)...(72)
 <223> Barley Alpha Amylase signal sequence.

<221> misc_feature
 <222> (73)...(1464)
 <223> K:trAPAOcDNA

<221> CDS
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> misc_feature
 <222> (73)...(75)
 <223> Added lysine residue

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ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
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gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
                10                      15                      20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
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gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac      240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
                45                      50                      55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc      288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
                60                      65                      70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act      336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
                75                      80                      85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
                90                      95                      100

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa      432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
                105                      110                      115                      120

ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac      480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp

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125										130					135					
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			140					145					150							
cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	576				
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala					
		155					160					165								
aac	cag	atc	aca	cgc	gct	ctg	ctc	ggg	gtg	gaa	gcc	cac	gag	atc	agc	624				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser					
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Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr					
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Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser					
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Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser					
265					270					275					280					
cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	ctg	960				
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu					
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ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	1008				
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg					
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gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	1056				
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser					
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ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	1104				
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr					
	330					335					340									
tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	1152				
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys					
345					350					355					360					

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Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu	
365 370 375	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag	1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu	
380 385 390	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg	1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly	
395 400 405	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag	1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys	
410 415 420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat	1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr	
425 430 435 440	
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg	1440
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<223> K:trAPAO translational fusion with barley alpha
 amylase signal sequence, for expression and
 secretion of the mature trAPAO in maize.

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 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
 25 30 35 40
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
 45 50 55
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
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 Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
 75 80 85
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro

90					95					100					
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
105					110					115					120
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
				125						130					135
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
			140						145						150
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
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Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
	170					175					180				
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
185					190					195					200
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
				205					210						215
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
			220					225					230		
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
		235				240						245			
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
	250					255					260				
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
265					270					275					280
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
				285					290						295
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
			300					305					310		
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
		315				320						325			
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
	330					335					340				
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
345					350					355					360
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
				365					370					375	
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
			380					385					390		
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
		395					400					405			
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
	410					415					420				
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr
425					430					435					440
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val
				445					450					455	
Ala	Ser	Leu	Val	Pro	Ala	Ala									
			460												

<210> 22
 <211> 1803
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1800)

<400> 22

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val 20 25 30	96
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro 35 40 45	144
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys 50 55 60	192
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr 65 70 75 80	240
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly 85 90 95	288
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val 100 105 110	336
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala 115 120 125	384
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val 130 135 140	432
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 145 150 155 160	480
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 165 170 175	528
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 180 185 190	576
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 225 230 235 240	720

225		230		235		240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg							768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala							
		245		250		255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa							816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln							
		260		265		270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc							864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe							
		275		280		285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta							912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val							
		290		295		300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc							960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile							
		305		310		315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt							1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser							
		325		330		335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa							1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys							
		340		345		350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca							1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro							
		355		360		365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca							1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala							
		370		375		380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa							1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys							
		385		390		395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt							1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe							
		405		410		415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc							1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile							
		420		425		430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg							1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp							
		435		440		445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc							1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile							
		450		455		460	

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala	
595 600	

<210> 23
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 23	
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	

	580	585	590
Val Ala Ser	Leu Val Pro Ala Ala		
595	600		

<210> 24
 <211> 3003
 <212> DNA
 <213> Unknown

<220>
 <223> Sequence is a barley alpha amylase signal
 sequence: esp1 mat: an artificial spacer sequence
 and K:trAPAO

<221> sig_peptide
 <222> (1)...(72)
 <223> Barley alpha amylase signal sequence

<221> misc_feature
 <222> (73)...(1575)
 <223> esp1 mat

<221> misc_feature
 <222> (1576)...(1611)
 <223> spacer sequence

<221> misc_feature
 <222> (1612)...(3000)
 <223> K:trAPAO

<221> CDS
 <222> (1)...(3000)

<221> misc_feature
 <222> (1612)...(1614)
 <223> Extra lysine

<400> 24

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	

ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct	96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala	
-5 1 5	

ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc	144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr	
10 15 20	

gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt	192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe	
25 30 35 40	

gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act	240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr	
45 50 55	

gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu	
60 65 70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	

285										290					295					
acg	act	ggt	gac	att	gct	cgt	gta	cct	gtt	ctc	gtc	ggg	acg	gtg	gcc	1008				
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala					
			300				305						310							
aac	gac	gga	ctt	ctc	ttt	gtc	ctc	ggg	gag	aat	gac	acc	caa	gca	tat	1056				
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr					
			315				320						325							
ctc	gag	gag	gca	atc	ccg	aat	cag	ccc	gac	ctt	tac	cag	act	ctc	ctt	1104				
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu					
			330				335						340							
gga	gca	tat	ccc	att	gga	tcc	cca	ggg	atc	gga	tcg	cct	caa	gat	cag	1152				
Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln					
345						350						355			360					
att	gcc	gcc	att	gag	acc	gag	gta	aga	ttc	cag	tgt	cct	tct	gcc	atc	1200				
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile					
			365						370						375					
gtg	gct	cag	gac	tcc	cgg	aat	cgg	ggt	atc	cct	tct	tgg	cgc	tac	tac	1248				
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr					
			380						385						390					
tac	aat	gcg	acc	ttt	gag	aat	ctg	gag	ctt	ttc	cct	ggg	tcc	gaa	gtg	1296				
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val					
			395						400						405					
tac	cac	agc	tct	gaa	gtc	ggg	atg	gtg	ttt	ggc	acg	tat	cct	gtc	gca	1344				
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala					
410						415						420								
agt	gcg	acc	gcc	ttg	gag	gcc	cag	acg	agc	aaa	tac	atg	cag	ggt	gcc	1392				
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala					
425						430						435			440					
tgg	gcg	gcc	ttt	gcc	aaa	aac	ccc	atg	aat	ggg	cct	ggg	tgg	aaa	caa	1440				
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln					
			445						450						455					
gtg	ccg	aat	gtc	gcg	gcg	ctt	ggc	tca	cca	ggc	aaa	gcc	atc	cag	gtt	1488				
Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val					
			460						465						470					
gac	gtc	tct	cca	gcg	aca	ata	gac	caa	cga	tgt	gcc	ttg	tac	acg	cgt	1536				
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg					
			475						480						485					
tat	tat	act	gag	ttg	ggc	aca	atc	gcg	ccg	agg	aca	ttt	ggc	gga	ggc	1584				
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly					
490						495						500								
agc	ggc	gga	ggc	agc	ggc	gga	ggc	agc	aaa	gac	aac	gtt	gcg	gac	gtg	1632				
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val					
505						510						515			520					

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755	2352

745	750	755	760	
tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa				2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	765	770	775	
aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt				2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	780	785	790	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc				2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	795	800	805	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg				2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	810	815	820	
cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc				2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	825	830	835	840
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att				2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	845	850	855	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc				2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	860	865	870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac				2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	875	880	885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc				2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	890	895	900	
gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat				2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	905	910	915	920
ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc				2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	925	930	935	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg				2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	940	945	950	
tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt				2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	955	960	965	
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Val Ala Ser Leu Val Pro Ala Ala	970	975		

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 Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 60 65 70
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
 75 80 85
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
 90 95 100
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
 105 110 115 120
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 125 130 135
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 140 145 150
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 155 160 165
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 170 175 180
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
 185 190 195 200
 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
 205 210 215
 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
 220 225 230
 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 235 240 245
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
 250 255 260
 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 265 270 275 280
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
 285 290 295
 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
 300 305 310
 Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
 315 320 325
 Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
 330 335 340
 Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln

345					350					355				360
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala
				365					370					375
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr
			380					385					390	
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu
		395					400					405		
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val
	410					415					420			Ala
Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly
425					430					435				440
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys
			445						450					455
Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln
			460						465					470
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr
		475					480							485
Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly
	490					495					500			
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp
505					510					515				520
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys
				525					530					535
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg
			540					545					550	Val
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr
		555					560					565		Ile
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu
	570					575								Val
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg
585					590					595				600
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr
				605					610					615
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu
			620					625					630	Ala
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu
	635						640					645		Gln
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser
	650					655					660			Phe
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly
665					670					675				680
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu
				685					690					695
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu
		700						705					710	Ser
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys
	715						720					725		Lys
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val
	730					735					740			Pro
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser
745					750					755				760
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser
				765					770					775
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr
			780					785					790	Phe
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser
	795						800					805		Ile
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp
														Trp

810		815		820											
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile
825					830					835					840
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile
			845							850				855	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser
			860					865					870		
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr
		875					880					885			
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile
	890					895					900				
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
905				910					915					920	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe
			925					930					935		
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
		940					945					950			
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
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 mature: artificial spacer: and K:trAPAO. For
 plant expression.

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ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc				96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	-5	1	5	
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc				144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	10	15	20	
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg				192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	25	30	35	40
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt				240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	45	50	55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc				288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	60	65	70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca				336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	75	80	85	
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc				384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	90	95	100	
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg				432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	105	110	115	120
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac				480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	125	130	135	
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc				528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	140	145	150	
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg				576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	155	160	165	
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg				624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	170	175	180	
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc				672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	185	190	195	200
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt				720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	205	210	215	

cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser 220 225 230	768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro 235 240 245	816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp 250 255 260	864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu 265 270 275 280	912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val 285 290 295	960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly 300 305 310	1008
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala 315 320 325	1056
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp 330 335 340	1104
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn 345 350 355 360	1152
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln 365 370 375	1200
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly 380 385 390	1248
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val 395 400 405	1296
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro 410 415 420	1344
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val 425 430 435 440	1392
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro 445 450 455 460	1440

445	450	455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc			1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg			
460	465	470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc			1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly			
475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc			1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser			
490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt			1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly			
505	510	515	520
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt			1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg			1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
540	545	550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat			1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
555	560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg			1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
570	575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa			1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag			1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg			1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
620	625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
635	640	645	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
650	655	660	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
665	670	675	680

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
685 690 695	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
700 705 710	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
715 720 725	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
730 735 740	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
745 750 755 760	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr	
765 770 775	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
780 785 790	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
795 800 805	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
810 815 820	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
825 830 835 840	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
845 850 855	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
860 865 870	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
875 880 885	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
890 895 900	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	

905	910	915	920	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag				2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	925	930	935	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt				2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	940	945	950	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca				2973
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	955	960	965	
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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	-5	1	5	
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	10	15	20	
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	25	30	35	40
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	45	50	55	
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	60	65	70	
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	75	80	85	
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	90	95	100	
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	105	110	115	120
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	125	130	135	
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	140	145	150	
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Leu Arg	155	160	165	
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	170	175	180	
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	185	190	195	200
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	205	210	215	
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	220	225	230	

Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro
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Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp
	250					255					260				
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu
265					270					275					280
Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val
				285					290					295	
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly
			300					305					310		
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala
		315					320					325			
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp
	330					335					340				
Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn
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Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
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2227-3615, K:trAPA0, extra lysine; 3616-3618, stop
codon. For bacterial expression.

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
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tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
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Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
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aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
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gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
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Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	
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Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly	
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Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr	

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			165					170						175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
		180					185					190			
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala

Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
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tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
	65				70					75					80		
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85					90					95			
gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt	336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
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ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
	145				150					155					160		
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165				170						175			
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180				185						190				
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Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
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Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210				215						220						
gga	tcc	ccg	gaa	ttc	acg	gat	ttt	ccg	gtc	cgc	agg	acc	gat	ctg	ggc	720	
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly		
	225				230					235					240		
cag	gtt	cag	gga	ctg	gcc	ggg	gac	gtg	atg	agc	ttt	cgc	gga	ata	ccc	768	
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro		
			245				250							255			
tat	gca	gcg	ccg	ccg	gtg	ggc	ggg	ctg	cgt	tgg	aag	ccg	ccc	caa	cac	816	
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His		
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ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala 325 330 335	1008
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ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc	1536

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Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu		
		515					520					525					
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Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro		
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Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly		
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Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala		
			565					570					575				
acg	ccc	aag	gaa	atg	gtc	gcg	cgc	atc	ttc	ggc	gac	aat	cag	ttc	aat	1776	
Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn		
		580					585					590					
cgg	ggg	gtc	tcg	gcc	ttc	tcg	gaa	gcg	ctt	gtg	cgc	cag	ggc	gcg	ccc	1824	
Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro		
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro		
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Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala		
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Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser		
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Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val		
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gtg	tcg	ccc	gga	cct	tcc	atc	ccc	cct	tgc	gcg	gat	ggc	gcc	aag	gcg	2160	
Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala		
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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn		
				725					730					735			

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Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
740 745 750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg	2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala	
755 760 765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc	2352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly	
770 775 780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac	2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
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Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
850 855 860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac	2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
865 870 875 880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct	2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
885 890 895	
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa	2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
900 905 910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala	
915 920 925	
acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat	2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr	
930 935 940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag	2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys	
945 950 955 960	
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att	2928

Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile	
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Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro	
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Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala	
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Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp	
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Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser	
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Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg	
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Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp	
1075 1080 1085	
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Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu	
1090 1095 1100	
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Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn	
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Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro	
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Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu	
1140 1145 1150	
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Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	
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 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
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 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
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 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
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 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
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 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
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 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
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 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
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 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
 225 230 235 240
 Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
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 Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
 260 265 270
 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
 275 280 285
 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
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 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
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 Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
 325 330 335
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 Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
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 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
 370 375 380
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln

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Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg
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Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu
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Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu
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Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala
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Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val
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Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro
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Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu
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Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp
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Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly
610						615				620	
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly
625				630						635	
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly
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Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp
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Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp
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Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly
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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
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Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser
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Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu
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Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln
	770					775				780	
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785				790						795	
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His
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Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala
			820					825			830
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser
		835					840			845	
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln

850		855		860
His Ser Leu Gln Asp	Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu Asp		
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Ser Val Ser Phe Ala	His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro Ala		
	885	890	895	
Val Leu Gly Val Ala	Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val Glu		
	900	905	910	
Ala His Glu Ile Ser	Met Leu Phe Leu Thr	Asp Tyr Ile Lys Ser Ala		
	915	920	925	
Thr Gly Leu Ser Asn	Ile Phe Ser Asp Lys	Lys Asp Gly Gly Gln Tyr		
	930	935	940	
Met Arg Cys Lys Thr	Gly Met Gln Ser Ile	Cys His Ala Met Ser Lys		
945	950	955	960	
Glu Leu Val Pro Gly	Ser Val His Leu Asn	Thr Pro Val Ala Glu Ile		
	965	970	975	
Glu Gln Ser Ala Ser	Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala Val		
	980	985	990	
Phe Arg Ser Lys Lys	Val Val Val Ser Leu	Pro Thr Thr Leu Tyr Pro		
	995	1000	1005	
Thr Leu Thr Phe Ser	Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu Ala		
	1010	1015	1020	
Glu Asn Ser Ile Leu	Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp Asp		
1025	1030	1035	1040	
Lys Pro Trp Trp Arg	Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser Ser		
	1045	1050	1055	
Cys Asp Pro Ile Ser	Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg		
	1060	1065	1070	
Gln Trp Ser Ile Thr	Cys Phe Met Val Gly	Asp Pro Gly Arg Lys Trp		
	1075	1080	1085	
Ser Gln Gln Ser Lys	Gln Val Arg Gln Lys	Ser Val Trp Asp Gln Leu		
	1090	1095	1100	
Arg Ala Ala Tyr Glu	Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala Asn		
1105	1110	1115	1120	
Val Leu Glu Ile Glu	Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala Pro		
	1125	1130	1135	
Ser Ala Val Tyr Gly	Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala Leu		
	1140	1145	1150	
Arg Thr Pro Phe Lys	Ser Val His Phe Val	Gly Thr Glu Thr Ser Leu		
	1155	1160	1165	
Val Trp Lys Gly Tyr	Met Glu Gly Ala Ile	Arg Ser Gly Gln Arg Gly		
	1170	1175	1180	
Ala Ala Glu Val Val	Ala Ser Leu Val Pro	Ala Ala		
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 <212> DNA
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 <223> GST:glyc(-)APAO open reading frame, 2490 nt; GST
 and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;
 mutation in putative glycosylation sites in bold
 and underlined, nt 1288-1290 (AAT->TCC) and nt
 1303-1305 (AGC->AAC).

<221> CDS
 <222> (1)...(2487)

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<221> misc_feature
<222> (688)...(2490)
<223> Glyc (-) APAO

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<222> (1288)...(1290)
<223> mutation in putative glycosylation site (AAT->TCC)

<221> mutation
<222> (1303)...(1305)
<223> mutation in putative glycosylation site (AGC->AAC)

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1          5          10          15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
          20          25          30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
          35          40          45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
          50          55          60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
          65          70          75          80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
          85          90          95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
          100          105          110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
          115          120          125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
          130          135          140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
          145          150          155          160

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gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca	720
Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro	
225 230 235 240	
aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac	768
Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp	
245 250 255	
gga ggg agg tat gtg aca ata gct gga cag att gga caa gac gct tcg	816
Gly Gly Arg Tyr Val Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser	
260 265 270	
ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc	864
Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala	
275 280 285	
aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc	912
Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val	
290 295 300	
acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc	960
Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr	
305 310 315 320	
gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct	1008
Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro	
325 330 335	
cct tgc acg ctg gtg cca gtg tcg gcc ttg tct tca cct gaa tac ctc	1056
Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu	
340 345 350	
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Phe Glu Val Asp Ala Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp	
355 360 365	
aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag	1152
Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu	
370 375 380	
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Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu	

385		390		395		400	
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Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro							
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ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc tcc gac agc							1296
Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser							
	420			425		430	
aac caa aac gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc							1344
Asn Gln Asn Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly							
	435			440		445	
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt							1392
Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly							
	450			455		460	
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt							1440
Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val							
	465			470		475	480
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa							1488
Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu							
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gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc							1536
Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu							
	500			505		510	
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct							1584
Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro							
	515			520		525	
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg							1632
Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val							
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gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt							1680
Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser							
	545			550		555	560
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag							1728
Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln							
	565			570		575	
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca							1776
Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser							
	580			585		590	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa							1824
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu							
	595			600		605	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc							1872
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala							
	610			615		620	

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Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
625 630 635 640	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	1968
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
645 650 655	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	2016
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
660 665 670	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	2064
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
675 680 685	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	2112
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	
690 695 700	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag	2160
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	
705 710 715 720	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa	2208
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	
725 730 735	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	2256
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	
740 745 750	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	2304
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	
755 760 765	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	2352
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	
770 775 780	
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Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser	
785 790 795 800	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga	2448
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg	
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			20				25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
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Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
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Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
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Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120						125		
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170					175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185					190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
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Gly	Ser	Pro	Glu	Phe	Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro
225					230					235					240
Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp
				245					250					255	
Gly	Gly	Arg	Tyr	Val	Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser
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Gly	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala
		275					280					285			
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Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr
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Ala	Ile	Gly	Asp	Gly	Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro
				325					330					335	
Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu
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Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp
		355					360					365			
Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu
	370					375					380				
Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu
385					390					395					400
Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro
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Asn	Gln	Asn	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly
		435					440					445			
Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly

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Ala Ser Ala Leu Ala	Glu Leu Leu Pro Val	Trp Ser Gln Leu Ile Glu		
	485	490	495	
Glu His Ser Leu Gln	Asp Leu Lys Ala Ser	Pro Gln Ala Lys Arg Leu		
	500	505	510	
Asp Ser Val Ser Phe	Ala His Tyr Cys Glu	Lys Glu Leu Asn Leu Pro		
	515	520	525	
Ala Val Leu Gly Val	Ala Asn Gln Ile Thr	Arg Ala Leu Leu Gly Val		
	530	535	540	
Glu Ala His Glu Ile	Ser Met Leu Phe Leu	Thr Asp Tyr Ile Lys Ser		
545	550	555	560	
Ala Thr Gly Leu Ser	Asn Ile Phe Ser Asp	Lys Lys Asp Gly Gly Gln		
	565	570	575	
Tyr Met Arg Cys Lys	Thr Gly Met Gln Ser	Ile Cys His Ala Met Ser		
	580	585	590	
Lys Glu Leu Val Pro	Gly Ser Val His Leu	Asn Thr Pro Val Ala Glu		
	595	600	605	
Ile Glu Gln Ser Ala	Ser Gly Cys Thr Val	Arg Ser Ala Ser Gly Ala		
	610	615	620	
Val Phe Arg Ser Lys	Lys Val Val Val Ser	Leu Pro Thr Thr Leu Tyr		
625	630	635	640	
Pro Thr Leu Thr Phe	Ser Pro Pro Leu Pro	Ala Glu Lys Gln Ala Leu		
	645	650	655	
Ala Glu Asn Ser Ile	Leu Gly Tyr Tyr Ser	Lys Ile Val Phe Val Trp		
	660	665	670	
Asp Lys Pro Trp Trp	Arg Glu Gln Gly Phe	Ser Gly Val Leu Gln Ser		
	675	680	685	
Ser Cys Asp Pro Ile	Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val Asp		
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Arg Gln Trp Ser Ile	Thr Cys Phe Met Val	Gly Asp Pro Gly Arg Lys		
705	710	715	720	
Trp Ser Gln Gln Ser	Lys Gln Val Arg Gln	Lys Ser Val Trp Asp Gln		
	725	730	735	
Leu Arg Ala Ala Tyr	Glu Asn Ala Gly Ala	Gln Val Pro Glu Pro Ala		
	740	745	750	
Asn Val Leu Glu Ile	Glu Trp Ser Lys Gln	Gln Tyr Phe Gln Gly Ala		
	755	760	765	
Pro Ser Ala Val Tyr	Gly Leu Asn Asp Leu	Ile Thr Leu Gly Ser Ala		
	770	775	780	
Leu Arg Thr Pro Phe	Lys Ser Val His Phe	Val Gly Thr Glu Thr Ser		
785	790	795	800	
Leu Val Trp Lys Gly	Tyr Met Glu Gly Ala	Ile Arg Ser Gly Gln Arg		
	805	810	815	
Gly Ala Ala Glu Val	Val Ala Ser Leu Val	Pro Ala Ala		
	820	825		